REMARKS

1. Formal Matters

a. Status of the Claims

Claims 1-20 are pending in this application. Claims 1-20 are hereby cancelled without prejudice to pursuing these claims in a continuing application. Claims 21-40 are new. Upon entry of these amendments, claims 21-40 are pending and under active consideration. Applicants respectfully request entry of the amendments and remarks made herein into the file history of the present application.

b. Amendments to the Claims

New claim 21 recites a nucleic acid consisting of 18 to 120 nucleotides, support for which may be found throughout the application including claims 1-3 as originally filed. New claim 21 also recites that the sequence of the nucleic acid may comprise (a) at least 18 consecutive nucleotides of SEQ ID NO: 3754, support for which may be found at paragraph 11159 of the application as originally filed. Paragraph 11159 recites:

> VGR411 folded precursor RNA is naturally processed by cellular enzymatic activity into at least 2 separate VGAM precursor RNAs, VGAM222 precursor RNA and VGAM223 precursor RNA, herein schematically represented by VGAM1 FOLDED PRECURSOR through VGAM3 FOLDED PRECURSOR, each of which VGAM precursor RNAs being a hairpin shaped RNA segment, corresponding to VGAM FOLDED PRECURSOR RNA of Fig. 1.

SEQ ID NOS: 208 and 209 represent the sequences of VGAM222 and VGAM223 respectively, each of which sequence is contained in the application as originally filed. VGAM222 (SEQ ID NO: 208) is located on the negative strand of the Vaccinia virus genome at positions 114,354 to 114,436. VGAM223 (SEQ ID NO: 209) is located on the negative strand of the Vaccinia virus genome at positions 114,571 to 114,650. Therefore, SEQ ID NO: 3754 (VGR411) represents the sequences of VGAM222 (SEQ ID NO: 208) and VGAM223 (SEQ ID NO: 209), and the intervening 134 base pairs in the Vaccinia virus genome between VGAM222 and VGAM223 (positions 114,437 to 114,570).

Claim 21 is also amended to recite that the nucleic acid may be: (b) an RNA equivalent of (a), support for which may be found at claim 1 and paragraphs 6648 and 6666 of the application as originally filed.

Claim 21 is also amended to recite that the nucleic acid may be: (c) a sequence at least 54/80 identical to (a) or (b), support for which may be found at claim 1, Table 1, lines 1459-1463, and paragraph 26993 of the application as originally filed. As described hereinabove, VGR411 (represented by SEQ ID NO: 3754) encodes VGAM223 (represented by SEQ ID NO: 209). VGAM223 forms a hairpin, as shown at Table 1, lines 1459-1463 and paragraph 26993 of the application as originally filed. The sequence of SEQ ID NO: 209 is 80 nucleotides in length. Within the predicted hairpin formed by the nucleic acid of SEQ ID NO: 209, 54 complementary nucleotides are paired.

Claim 21 is also amended to recite that the nucleic acid may be: (d) the complement of any one of (a)-(c), support for which may be found at claim 1 and paragraphs 6648 and 6666 of the application as originally filed..

New claim 22 recites the nucleic acid of claim 21, wherein the at least 18 nucleotides is of a sequence selected from the group consisting of SEQ ID NOS: 208 and 209, support for which can be found at Table 1, lines 1452-1456 and 1459-1463, and paragraphs 6647 and 6665 of the application as originally filed.

New claim 23 recites a nucleic acid of claim 21, wherein the at least 18 nucleotides is of a sequence selected from the group consisting of SEQ ID NOS: 557 and 558, support for which can be found at Table 1, lines 1452-1456 and 1459-1463, and paragraphs 6649 and 6667 of the application as originally filed.

New claim 24 recites a nucleic acid of claim 21, wherein the nucleic acid consists of 18 to 24 nucleotides, support for which can be found at claim 1 as originally filed.

New claim 25 recites a nucleic acid with a sequence consisting of (a) SEQ ID NO: 3754 (b) an RNA equivalent of (a); (c) a sequence at least 54/80 identical to (a) or (b); or (d) the complement of any one of (a)-(c), support for which may be found at new claim 21.

New claim 26 recites a nucleic acid of claim 25, wherein the at least 18 nucleotides is of a sequence selected from the group consisting of SEQ ID NOS: 208 and 209, support for which can be found at new claim 22.

New claim 27 recites a nucleic acid of claim 25, wherein the at least 18 nucleotides is of a sequence selected from the group consisting of SEQ ID NOS: 557 and 558, support for which can be found at new claim 23.

New claim 28 recites a nucleic acid of claim 25, wherein the nucleic acid consists of 18 to 24 nucleotides, support for which can be found at new claim 24.

New claim 29 recites a nucleic acid of claim 22, wherein the nucleic acid is an RNA, support for which can be found at claim 1 as originally filed and at paragraphs 6648 and 6666 of the application as originally filed.

New claim 30 recites a nucleic acid of claim 26 wherein the nucleic acid is an RNA, support for which can be found at claim 1 as originally filed and at paragraphs 6648 and 6666 of the application as originally filed.

New claim 31 recites a nucleic acid of claim 29, wherein the nucleic acid is capable of modulating expression of a target gene, support for which can be found at claim 3 as originally filed.

New claim 32 recites a nucleic acid of claim 30, wherein the nucleic acid is capable of modulating expression of a target gene, support for which can be found at claim 3 as originally filed.

New claim 33 recites a nucleic acid of claim 31, wherein the nucleic acid is at least 17/21 complementary to a binding site sequence of 18 to 24 nucleotides of a target gene and wherein the binding site sequence is located in an untranslated region of RNA encoded by the target gene. Table 2, lines 11663-11682 shows that among all listed target binding sites of the nucleotide represented by SEQ ID NO: 558, the sequence of which is included in the sequence of SEQ ID NO: 209, at the lowest level of complementarity a target binding site of 21 nucleotides has 17 nucleotides complementary to the sequence of SEQ ID NO: 558; and (b) that the binding site sequence is located in an untranslated region of RNA encoded by the target gene, support for which can be found at paragraphs 22, 6659, and 6679 of the application as originally filed.

New claim 34 recites a nucleic acid of claim 32, wherein the nucleic acid is at least 17/21 complementary to a binding site sequence of 18 to 24 nucleotides of a target gene and wherein the binding site sequence is located in an untranslated region of RNA encoded by the target gene, support for which can be found at new claim 33.

New claim 35 recites a vector comprising an insert, wherein an insert consists of the nucleic acid of claim 21, support for which can be found at paragraph 24 of the application as filed.

New claim 36 recites a vector comprising an insert, wherein an insert consists of the nucleic acid of claim 25, support for which can be found at paragraph 24 of the application as filed.

New claim 37 recites a probe comprising an insert, wherein an insert consists of the nucleic acid of claim 21, support for which can be found at paragraph 28 of the application as filed.

New claim 38 recites a probe comprising an insert, wherein an insert consists of the nucleic acid of claim 25, support for which can be found at paragraph 28 of the application as filed.

New claim 39 recites a gene expression inhibition system comprising the vector of claim 35 and a means for inserting said vector into a cell, support for which can be found at paragraph 27 as originally filed.

New claim 40 recites a gene expression inhibition system comprising the vector of claim 36 and a means for inserting said vector into a cell, support for which can be found at paragraph 27 as originally filed.

c. Amendments to the Specification

Paragraph 0145 is amended to assign SEQ ID NO: 3751 to the sequence shown in Fig. 12A in compliance with 37 C.F.R. § 1.821-1.825.

Paragraph 0150 is amended to assign SEQ ID NOS: 3755-3760 to the listed in sequences in compliance with 37 C.F.R. §§ 1.821-1.825. Paragraph 0150 is also amended to correct typographical errors.

Paragraph 0156 is amended to assign SEQ ID NO: 3752 to the sequence shown in Fig. 13A in compliance with 37 C.F.R. §§ 1.821-1.825.

Paragraph 0159 is amended to assign SEQ ID NO: 3753 to the sequence shown in Fig. 14A in compliance with 37 C.F.R. §§ 1.821-1.825.

d. Elections/Restrictions

At pages 2-4 of the Office Action, the Examiner requires restriction to one of the following inventions under 35 U.S.C. § 121:

1. Claims 1-8, 12, and 14, drawn to a viral gene and vectors comprising the gene.
2. Claims 9 and 10, drawn to a method of inhibiting translation by use of a viral gene.

3. Claim 13, drawn to a method of using a probe.
4. Claims 15-20, drawn to an antiviral compound and method of use.

Applicant elects without traverse Group 1, which now is considered claims 21-40, drawn to an isolated nucleic acid, a vector comprising said nucleic acid, a probe comprising said nucleic acid, and a gene expression inhibition system comprising said vector and a means for inserting said vector into a cell.

At page 4 of the Office Action, the Examiner requires election of a single disclosed target gene species for Group 1 under 35 U.S.C. § 121. Applicant elects without traverse target gene EIF2C1 which has the sequence of SEQ ID NO: 1413. New claims 31-34 read on the elected target gene.

At page 5 of the Office Action, the Examiner requires election of a single nucleic acid sequence for the elected Group. Applicant elects with traverse nucleic acids related to SEQ ID NO: 3754.

The Examiner is permitted under 35 U.S.C. 121 to issue a restriction requirement between independent and distinct inventions. However, the Director has partially waived the requirements of 37 C.F.R. § 1.141 *et seq.* to permit a reasonable number of nucleotide sequences to be claimed in a single application. *See* Examination of Patent Applications Containing Nucleotide Sequence, 1192 O.G. 68 (November 19, 1996). It has been determined that normally **ten** sequences constitute a reasonable number for examination purposes absent an exceptional case. *See* MPEP 803.04.

The Examiner has failed to demonstrate that the claimed sequences are an exceptional case necessitating that the number of sequences to be selected be less than ten. Applicant respectfully submits that the Examiner is impermissibly disregarding the waiver of 37 C.F.R. § 1.141 *et seq.* Accordingly, Applicant respectfully requests reconsideration of the restriction requirement and the opportunity to elect up to ten sequences for further prosecution.

2. Conclusion

Applicant respectfully submits that the instant application is in good and proper order for allowance and early notification to this effect is solicited. If, in the opinion of the Examiner, a telephone conference would expedite prosecution of the instant application, the Examiner is encouraged to call the undersigned at the number listed below.

Respectfully submitted,

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